

Human A4 Receptor

120	240 40	360	480	600	720	840 240	960 280	108(320	1200	1320	1440 421
1 TTGAGCCGGCAGACTGCGAAAAGTAGCTGGAGCCGGAGCAGGAGCAGAACCTGTTGCTGCAGACGGGCTTGGTGGATTCCTGCCGCCGACAGGGCTCGCCGGGAGGTTCATC	121 ATGAATGAGAAATGGGAACACAAACTCTGGAATGTCAATGTCAATGACAACATCATCATCTGTACTCAGATATTAATATTACCTATGTGAACTACTATCTTCAC 1 M N E K W D T N S S E N W H P I W N V N D T K H H L Y S D I N I T Y V N Y Y L H	241 CAGCCTCAAGTGGCAGCAATCTTCATTATTTCTGATCTTCTTTTTTTT	361 AATCTCTTCATCTTAAACCTGGCCATAAGTGATTTACTAGTAGGCATATTCTGCATGCCTATAACACTGCTGGACAATATTATAGCAGGA θ GGCCATTTGGAAACACGATGCCAAGATC 81 N L F I L N L A I S D L L V \cdot G I F C M P I T L L D N I I A G W P F G N T M C K I	481 AGTGGATTGGTCCAGGGAATATCTGTCGGTCTTTACGTTAGTTGCTGTAGATAGGTTCCAGTGTGTGGGTCTACCCTTTTAAACCAAAGCTCACTATCAAGACAGCG 121 S G L V Q G I S V A A S V F T L V A I A V D R F Q C V V Y P F K P K L T I K T A	601 TITCTCATTATTATGATCATCGGTCCTAGCCATCACCATTATGTCTCCCAGTAATGTTACATGTGCAAGAAAAATATTACCGAGTGAGACTCAACTCCCAGAATAAAACC 161 F V I M I I W V L A I T I M S P S A V M L H V Q E E K Y Y R V R L N S Q N K T	721 AGTCCAGTCTACTGGTGCCGGAAGACTGGCAAATGAGGAAGATCTACACCACTGTGGTTTGCCAACATCTACCTGGCTCCCCTCTCCCTCATGTCATGTATGGA 201 S P V Y W C R E D W P N Q E M R K I Y T T V L F A N I Y L A P L S L I V I M Y G	95°S 241 R I G I S L F R A A V P H I G R K N Q E Q W H V V S R K K Q K I I K M L L I V A	961 CTGCTTTTTATTCTCTCATGGCTGCCCCTGTGGACTCTAATGATGCTCTCAGACTTCTCCAAATGAACTGCAGATCATCAACATCTACATCTACCTTTTGCACACTGG 281 L L F I L S W L P L W T L M M L S D Y A D L S P N E L Q I I N I Y I Y P F A H W	1081 CTGGCATTCGGCAACAGCAGTGTCCATCATTTATGGTTTCTTCAACGAGAATTTCCGCCGTGGTTTCCAAGAAGCAAGC		1321 AAACCCCAACAGGAATTAGTGATGGAAGAATTAAAAGAAGTCTACTAACAGGGGTTTAAAAAGAGCTAGTGATAATCCTAACTGCTACTACGATTATATATTTAAATCCATTGC 401 K P Q Q E L V M E E L K E T T N S S E I *
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TM1 47-69
TM2 82-104
TM3 121-141
TM4 160-182
TM5 218-240
TM6 275-297
TM7 312-336

Figure 1

Amino Acid Homologies of A4 and Related Mammalian Receptors

Note: All sequences are human

Numbers below represent % similarity / % identity

l	Mu	NK1	CCKA	Gastrin	Y5	Y4	Y2	Y1	Orexin2	Orexin1	A4
A4	62/25	55/26	63/31	61/28	61/28	59/28	61/30	63/31	61/32	59/32	100
Orexin1	58/26	59/32	59/30	58/27	61/26	64/32	59/32	58/26	84/69	100	. 4
Orexin2	58/28	56/31	58/29	61/29	59/26	63/32	60/31	60/27	100		
Y1	54/24	54/29	56/28	60/30	66/32	71/43	63/31	100			
Y2	57/24	59/30	56/29	56/27	63/32	62/33	100				•
Y4	54/25	53/26	56/28	54/29	64/29	100					
Y5	61/26	57/24	55/26	58/28	100						
Gastrin	58/24	55/27	73/50	100							i nite
CCKA	55/26	57/30	100								
NK1	60/26	100								•	2 mag
Ми	100										1,5

Legend:

Code:	GenBank Assession No.	Description
93		
Orexin 1	AF041243	Human Orexin receptor-1
Orexin2	AF041245	Human Orexin receptor-2
	P25929	Human Neuropeptide receptor Type1
Y1 - Y2 - X	P49146	Human Neuropeptide receptor Type2
Y4-	P50391	Human Neuropeptide receptor Type4
Y4 Y5	U56079	Human Neuropeptide receptor Type5
Gastrin	P32239	Human Gastrin/Cholecytokinin Type B receptor
CCKA	P32238	Human Cholecystokinin Type A receptor
NK1	P25103	Human Neurokinin-1 / Substance-P receptor
Mu	P35372	Human Mu-type opioid receptor

Data above was obtained using the GAP program from the WISCONSIN PACKAGE Version 9.0

Parameters used:

Symbol comparison table: oldpep.cmp *

Gap Creation Penalty:

30

Gap ExtensionPenalty:

* This is the default scoring matrix used by versions of the Wisconsin Package prior to Version 9.0. based on hte PAM250 table from M. Dayhoff¹.

1.) Schwartz, R. M. and Dayhoff, M. O. [1979]. Matrices for Detecting Distant Relationships. In Atlas of Protein Sequence and Structure, (M.O. Dayhoff, ed.), 5, Suppl. 3, (pp; 353-358), National Biomedical Research Foundation, Washington D.C., USA.

A4 vs. Human Y1 receptor

Percent Similarity: 63.032 Percent Identity: 30.585

1	MNEKWDTNSSENWHPIWNV.NDTKHHLYSDINXTYVNYYLHQPQVAAIFI	49
1	- :.: :. : : .:.: ::.:: : MNSTLFSQVENHSVHSNFSEKNAQLLAFENDDCHLPLAMI	40
50	ISXFLIFFLCMMGNTVVCFIVMRNKHMHTVTNLFILNLAISDLLVG	95
41	:. ::: .: .:.: ::: : : :: : :: :: ::	90
96		145
91	: : : ::::: :: ::	140
146	CVVYPFKPKLTIKTAFVIIMIIWVLAITIMSPSAVMLHVQEEKYYRVRLN	195
141	:: : . : : : : : : .: . : LIINPRGWRPNNRHAYVGIAVIWVLAVASSLPFLIYQVMTDEPFQNVTLD	190
196	SQNKTSPVYWCREDWPNQEMRKIYTTVLFANIYLAPLSLIVIMYGRIGIS	245
191	: : ::: .:.	237
246	LFRAAVPHTGRKNQEQWHVVSRKKQKIIKMLLIVALLFILSWLPLWTLMM	295
238	:::.: :: ::: :: .: LKRRNNMMDKMRDNKYRSSETKRINIMLLSIVVAFAVCWLPLTIFNT	284
296	LSDYADLSPNELQIINIYIYPFAHWLAFGNSSVNPIIYGFFNENFR	341
285	: :.:	328
342	RGFQEAFQLQLCQKRAKPMEAYTLKAKSHVLINTSNQLVQESTFQNPHGE	391
329	:: ::: : :: :: :: :: :: RDLQFFFNFCDFRSRD.DDYETIAMSTMHTDVSKTSLKQAS	368
	TLLYRKSAEKPQQELVMEELKETTNSSEI* 421	
	.: :: .::.:: : PVAFKKINNNDDNEKI*	

Amino Acid Comparison

Human A4 Receptor vs. Human Orexin Receptor-2

Percent Similarity: 60.500 Percent Identity: 31.500

Gap Weight: 30 Length Weight: 1

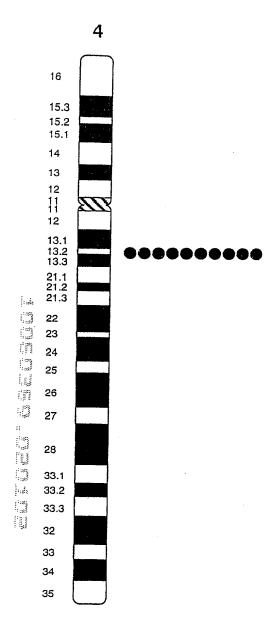
Top sequence: Human Orexin receptor-2
Bottom Sequence: Human A4 receptor

	MSGTKLEDSPPCRNWSSASELNETQEPFLNPTDYDDEEFLRYLWREYLHP	
1	MNEKWDTNSSENWHPIWNVNDTKHHLYSDINXTYVNYYLHQ	41
51	KEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNHHMRTVTNYFIVNLSLAD .: .:: : ::: .:: .: . .	100
42	PQVAAIFIISXFLIFFLCMMGNTVVCFIVMRNKHMHTVTNLFILNLAISD	91
101	VLVTITCLPATLVVDITETWFFGQSLCKVIPYLQTVSVSVLTLSCIAL : : : : : : :	150
92	LLVGIFCMPITLLDNIIAGWPFGNTMCKISGLVQGISVAASVFTLVAIAV	141
151	DRWYAICHPLMFKSTAKRARNSIVIIWIVSCIIMIPQAIVMECST	195
142	DRFQCVVYPFKPKLTIKTAFVIIMIIWVLAITIMSPSAVMLHVQEEKYYR	191
196	VFPGLANKTTLFTVCDERWGGEIYPKMYHICFFLVTYMAPLCLMVLAYLQ	245
192	VRLNSQNKTSPVYWCREDWPNQEMRKIYTTVLFANIYLAPLSLIVIMYGR	241
246	<pre>ifrklwcrqipgtssvvqrkwkplqpvsqprgpgqptksrmsavaAeikq . : .: : . : :</pre>	295
242	IGISLFRAAVPHTGEKNQEQWHVV	Ź65
296	<pre>IRARRKTARMLMVVLLVFAICYLPISILNVLKRVFGMFAHTEDRETVYAW :: :: :: :: :: :: </pre>	345
266	SRKKQKIIKMLLIVALLFILSWLPLWTLMMLSDYADLSPNELQIINIYI.	314
346	FTFSHWLVYANSAANPIIYNFLSGKFREEFKAAFSCCCLGVHHRQEDRLT	395
315	:. : .:: :. : ::: : :. .:::::. YPFAHWLAFGNSSVNPIIYGFFNENFRRGFQEAFQLQLCQKRAKPME	361
396	RGRTSTESRKSLTTQISNFDNISKLSEQVVLTSI : :.	429
362	AYTLKAKSHVLINTSNQLVQESTFQNPHGETLLYRKSAEKPQQELVMEEL	411
430	STLPAANGAGPLQNW* 445	
412	KETTNSSEI* 421	

A4 vs. Human CCK receptor

Percent Similarity: 63.514 Percent Identity: 31.081

1	MNEKWDTNSSENWHPIWNVNDTKHHLYSDINXTYVNYYLHQPQV	44
1	: ::: : : :: : : . MDVVDSLLVNGS	39
45	. AAIFIISXFLIFFLCMMGNTVVCFIVMRNKHMHTVTNLFILNLAISDLL	93
40	: : : : ::: : . ::: : : : : :	89
94	VGIFCMPITLLDNIIAGWPFGNTMCKISGLVQGISVAASVFTLVAIAVDR	143
90	::: :: ::: .:: .:: .:: .:: LCLFCMPFNLIPNLLKDFIFGSAVCKTTTYFMGTSVSVSTFNLVAISLER	139
144	FQCVVYPFKPKLTIKTAFVIIMIIWVLAITIMSPSAVMLHVQEEKYYR	191
140	::. ::::: . :: . . :: . :: :: YGAICKPLQSRVWQTKSHALKVIAATWCLSFTIMTPYPIYSNL	182
192	VRLNSQNKTSPVYWCREDWPNQEMRKIYTTVLFANIYLAPLSLIVIMYGR	241
183	.:: : .: : : ::: :::: VPFTKNNNQTA.NMCRFLLPNDVMQQSWHTFLLLILFLIPGIVMMVAYGL	231
242	IGISLFRAAVPHTGRKNQEQWHVVSRK	268
232	::. ::: :. :: :. :sLelyQgikfeasQkksakerkpsttssgkyedsdgcylQktrpprkle	
269		292
282	::: : :::: : :::: LRQLSTGSSSRANRIRSNSSAANLMAKKRVIRMLIVIVVLFFLCWMPIFS	331
293	LMMLSDYADLSPNELQIINIYIYPFAHWLAFGNSSVNPIIYGFFNENFRR	342
332	: :: :: : :	379
343	GFQEAFQLQLCQKRAKPMEAYTLKAKSHVLINTSNQLVQESTFQNPHGET	392
380	.: :: :: :: :: :: :: :: :: :: :: :: ::	416
	LLYRKSAEKPQQELVMEELKETTNSSEI* 421	
417	. :. . . SYSHMSASVPPQ 428	



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